

# B110: Genomics and its Impact on Society

## Educators' Professional Development Day

### 3/23/07

## Hands-On Exercise: Grain Yield after Milling

Begin on the web at [www.gramene.org](http://www.gramene.org)

You want to increase the yield of rice after milling.

What is some of the current literature on this topic?

[Literature Home](#) | [Rice Genetics Newsletters](#) | [Tutorial](#) | [FAQ](#)

Literature search

Search for publications:

[ e.g. Wessler SR , rice genome , Rice Genetics Newsletter ]

Items 1 to 3 of 3

- 1. Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z**  
 Molecular mapping of QTLs for rice **milling yield** traits. ([More info](#)) [Reference ID: 7776]  
 Acta-Genetica-Sinica, 2002, vol.29, pp791-797
- 2. Parker-G-D, Chalmers-K-J, Rathjen-A-J, Langridge-P**  
 Mapping loci associated with **milling yield** in wheat (Triticum aestivum L.) ([More info](#)) [Reference ID: 11306]  
 Molecular Breeding, 1999, vol.5, pp561-568
- 3. Martinez-Bustos-F, Delgado-L-L, Victorio-M-G, Morales-S-E**  
 Characterization of yellow rice and development of instant flours by hydrothermal process ([More info](#)) [Reference ID: 2649]  
 Archivos latinoamericanos de nutricion, 1997, vol.47, pp50-56

You should look to see what ‘associations’ there are in the database with an article. Click on “More Info” for the first article. There are 3 QTL associated with this article.

➔ a. **Select the QTL for more information on them** (*click on ‘QTLs (3)’* )..

Search result	
Reference ID	7776
Title	Molecular mapping of QTLs for rice milling yield traits.
Source	Acta-Genetica-Sinica , 2002, 29, pp.791-797
Authors	Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z
Abstract	QTLs of three milling yield traits, including brown rice (BR, %), milled rice (MR, %) and head milled rice (HR, %) ,were mapped using a set of 212 Lemont/Teging RI population, an RFLP linkage map with 182 markers and a mixed model approach (QTLMapper V1.0). The population showed continuous distributions with transgressive segregation on both sides for all traits while HR had a wider variation than BR and MR. One and four main effect QTLs were detected for MR and HR. Two QTLs for HR (QHr6 and QHr7) had large additive effects. Twelve five and sixteen pairs of digenic epistatic loci were associated with BR, MR and HR respectively. Epistasis was more important than main effect QTLs according to the mapping results. A complex relationship was observed for epistatic pairs mapped in same trait or among different traits by sharing intervals.
Cross-reference	Not available
Associated Data	<a href="#">QTLs (3)</a> <a href="#">Markers (3)</a>

This will bring up a table that lists those three QTL, and following those links will provide more information. Looking at the Trait Name can help you understand the traits of interest. In this case, it is milled rice.

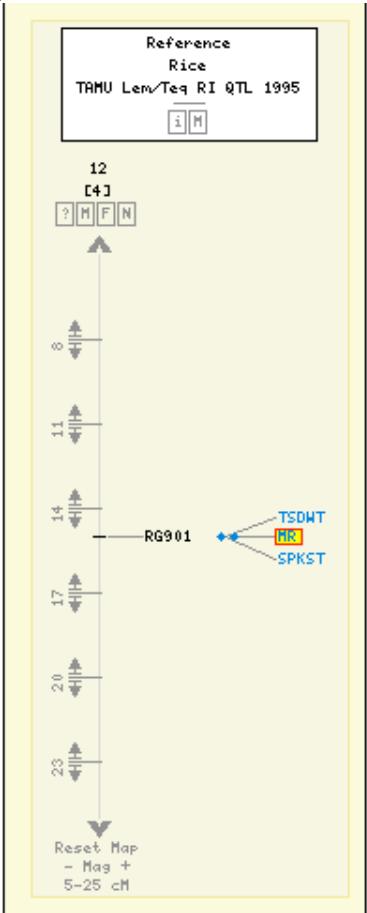
Reference ID	7776			
Title	Molecular mapping of QTLs for rice milling yield traits.			
Associated QTL	Accession	Trait Symbol	Trait Name	Published Symbol
	<a href="#">AQL002</a>	HEADR	head rice	QHr2
	<a href="#">AQL004</a>	HEADR	head rice	QHr6
	<a href="#">AQL001</a>	MR	milled rice ratio	QMri2

➔ b. **Select AQL001 to get more information.**

You will be able to select the link to view this QTL on a map. Note that there are synonyms, that it is a Quality trait, and that it is on Chromosome 12.

Details for QTL "AQL001" (milled rice ratio)										
QTL Accession ID	AQL001									
Species	Oryza sativa (Rice)									
Trait Symbol	MR									
Trait Name	milled rice ratio									
Published Symbol	QMr12									
Trait Synonym(s)	milled rice milled rice percentage									
Trait Category	Quality									
Chromosome	12									
Mappings	Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Method	
	Oryza sativa (Rice)	QTL	TAMU Lem/Teq RI QTL 1995	MR	12		15	15	<a href="#">View in MapInfo DB</a> <a href="#">View Comparative Map</a>	Experimental
Related Ontologies	Term Type			Term				Evidence	Reference	
	Trait Ontology			milled rice ( <a href="#">TO:0000144</a> )				IAGP	<a href="#">Gramene Lit. 7776</a>	
	Plant Structure			seed ( <a href="#">PO:0009010</a> )				IC	<a href="#">Gramene Lit. 11453</a>	
	Plant Growth and Development Stage			FR.04 fruit ripening complete ( <a href="#">PO:0007038</a> )				IC	<a href="#">Gramene Lit. 11453</a>	
	Species Ontology			Oryza sativa ( <a href="#">GR_tax:013681</a> )				SM	<a href="#">Gramene Lit. 7776</a>	
Comments	Trait was related with grain quality.									
DBXRefs	<b>Gramene Literature</b> <a href="#">Mei-H Luo-L Guo-L Wang-Y Yu-X Ying-C Li-Z, Molecular mapping of QTLs for rice milling yield traits., Acta-Genetica-Sinica, 29, 2002, pp. 791-797</a>									

➡ 2) Select “View Comparative Map to view it on the QTL map.



You can play with the map, Click on “reset map” to view the entire map. Become familiar with the map legend. But keep in mind that each redraw of the map may take several seconds to render.

Feature Types:

- QTL
- RFLP

Menu Symbols:

- Map Set Info
- Map Details
- Matrix View
- Limit to One Map
- Delete Map Set
- Delete Map
- Flip Map
- Unflip Map
- New Map View

CMap v0.16

➡ a. Select the Trait Accession for ‘milled rice ratio.’ (Click on “TO:0000144”)

Ontologies show relationships between terms, and this reflects that milled rice (ratio) is an example of seed quality, which is an example of a quality trait. There are 8 QTL that are associated with the MR trait, which we will come back to in a minute.

First, however, you should know that sometimes it can be helpful to explore related terms so that we can consider other terms to search for.

Summary for TO Term: <i>milled rice</i> (TO:0000144)	
Term Name	milled rice
Synonym	milled rice ratio, MR.
Aspect	Trait
Derivation	
<ul style="list-style-type: none"> <li>• <a href="#">trait ontology (TO:0000387)</a> #10679 <ul style="list-style-type: none"> <li>◦ [i] <a href="#">quality trait (TO:0000597)</a> #963 <ul style="list-style-type: none"> <li>▪ [i] <a href="#">seed quality (TO:0000162)</a> #907 <ul style="list-style-type: none"> <li>▪ [i] <a href="#">milled rice (TO:0000144)</a> #8</li> </ul> </li> </ul> </li> </ul> </li> </ul>	
Parent Term (1)	
<ul style="list-style-type: none"> <li>• [i] <a href="#">seed quality (TO:0000162)</a></li> </ul>	
Total Number of Annotations:	8 objects, 8 associations
QTL:	<a href="#">Oryza sativa QTL</a>

➔ b. Select the parent term of milled rice. (Click on “seed quality (TO:0000162).”)

More terms are revealed that are also associated with seed quality. Many of these will also affect milling yield, so in further research you may wish to explore some of these other options.

➔ c. Go back to “Milled Rice”. AT the bottom of the page is a link to the 8 associated QTL. Click on it.

QTLs 1 to 8 of 8									
<a href="#">[ Download Data ]</a>									
QTL Accession ID	Species Name	Trait Symbol	Trait Name	Published Symbol	Trait Synonyms	Trait Category	Linkage Group	Map	Position
<a href="#">AQL001</a>	Oryza sativa	MR	milled rice ratio	QMr12	milled rice, milled rice pe...	Quality	12	Oryza sativa-TAMU Lem/Taq RI QTL 1995-12	15-15 cM
<a href="#">CQR2</a>	Oryza sativa	MR	milled rice ratio		milled rice, milled rice pe...	Quality	3	Oryza sativa-CNHZAU Zh97/Ming63 RI QTL 2002-3	88.1-94.4 cM
<a href="#">CQR3</a>	Oryza sativa	MR	milled rice ratio		milled rice, milled rice pe...	Quality	5	Oryza sativa-CNHZAU Zh97/Ming63 RI QTL 2002-5	114.4-127.6 cM
<a href="#">AQEE012</a>	Oryza sativa	MR	milled rice ratio		milled rice, milled rice pe...	Quality	10	Oryza sativa-Cornell IR64/IRG105 QTL 2003-10	0-54.9 cM
<a href="#">AQFU013</a>	Oryza sativa	MR	milled rice ratio	mr5	milled rice, milled rice pe...	Quality	5	Oryza sativa-LSU Caiapo/IRGC103544 QTL 2004-5	50-63 cM
<a href="#">AQFU014</a>	Oryza sativa	MR	milled rice ratio	mr7	milled rice, milled rice pe...	Quality	7	Oryza sativa-LSU Caiapo/IRGC103544 QTL 2004-7	0-8 cM
<a href="#">AQFU048</a>	Oryza sativa	MR	milled rice ratio		milled rice, milled rice pe...	Quality	11	Oryza sativa-LSU Caiapo/IRGC103544 QTL 2004-11	63-63 cM
<a href="#">AQFU049</a>	Oryza sativa	MR	milled rice ratio		milled rice, milled rice pe...	Quality	11	Oryza sativa-LSU Caiapo/IRGC103544 QTL 2004-11	77-77 cM

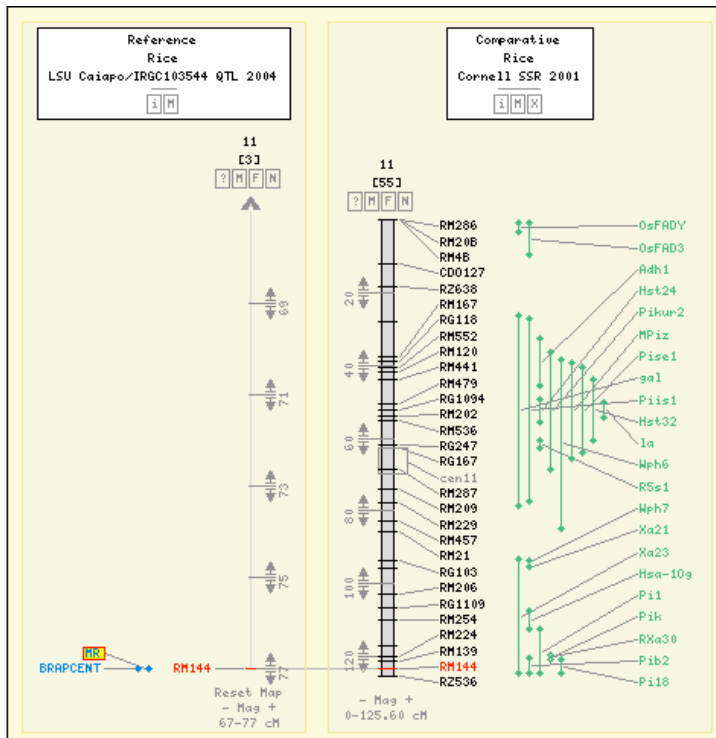
➔ 3) For this exercise, select **AQFU049**. (In most cases you may wish to review all 8 of these QTL to learn what data is known about them.)

Once again you can see that this is a rice QTL for milled rice ratio. You can also learn that it is on chromosome 11. If you would like more reference information for this QTL you should select the literature reference link, since it is different than the previous article we reviewed.

a. View the QTL map for “AQFU049” (Click on “View comparative Map”)

➡ 4) Return to the Cmap view in #6 (click the browser's 'Back' button three times.)

Compare this map to a genetic map to see what other features may be in the same region. (Genetic maps will give a general order to surrounding features, but do not offer the exact sequence and distance. Underneath the map select 'Show Reference Menu.' We will put the comparison map on the right, so under the appropriate heading select the 'Select Map Set' menu to open a list of maps with comparisons. Click on "Genetic: Rice – Cornell SSR 2001. If there were more than one chromosome with correlations you would need to select the ones you wanted to compare. In this case, the only comparisons are on chromosome 11. Click on 'Redraw Map.')



You will see that the marker that is associated with your QTL is also located near several other markers and some interpolated genes. Once again, following those links will provide more information that may or may not be useful or interesting to you.

➡ 5) (Optional if time permits) Use the CMAP tools to alter the view or select another comparison map.  
a. Crop the maps to magnify the view (Click on the arrows for cropping.)

Use "options" and "additional options" menus. (Located below the map image. Click on 'Show Options Menu' and "Show Additional Options Menu")

6) Now you will view "RM144" marker detail information. (Click on 'RM144')

➡ a. We can see that this marker has been mapped to several different maps and map types. To get other marker detail info, you need to go to the markers module detail page. (Select the first "View Oryza sativa SSR marker "RM144" in Marker DB" to view the marker in the markers module.)

Maps Home | Maps | Map Search | Feature Search | Matrix | Map Sets | Feature Types | Map Types | Evidence Types | Species | Saved Links | Help | Tutorial | FAQ

**Feature "RM144"**

Feature Name: RM144 [View Alias Details]  
 Aliases: X87711  
 Accession ID: wip2005a-97 [View Feature Type Info]  
 Feature Type: SSR  
 Species: Rice  
 Map: Map Set: LSU Caiapo/IRGC103544 QTL 2004 [View Map Details]  
 Map Name: 11  
 Start: 77.00 cM  
 Stop: 77.00 cM  
 Cross-reference: [Oryza sativa SSR "RM144" details](#)

Feature	Accession	Map	Map Type	Aliases	Evidence Type	Actions
RM144	wip2005a-11-6887	Rice-Class I SSR (9-11) 2005-11	Sequence	X87711	Marker Identity	[Correspondence Details] [View On Map] [Comparative View]
RM144	wip2005b-11-11249	Rice-Class I SSR (IRGSP) 2005-11	Sequence	X87711	Marker Identity	[Correspondence Details] [View On Map] [Comparative View]
RM144	wip2005a-11-11283	Rice-Class I SSR (IRGSP) 2005-11	Sequence	X87711	Marker Identity	[Correspondence Details] [View On Map] [Comparative View]
RM144	fcc2005a-025	Rice-CNHAU Zhan971 H94 QTL 2005-11	QTL	X87711	Marker Identity	[Correspondence Details] [View On Map] [Comparative View]

You are now in the Markers Database (look at the module heading). There are several navigation tabs along the top of your information. Click on the Associations tab.

## Search

Name:  Type:  Species:

E.g., "AG840697,AG841134", "rm", Oat RFLPs like "CDO", or view help.

### View Rice SSR "RM144"

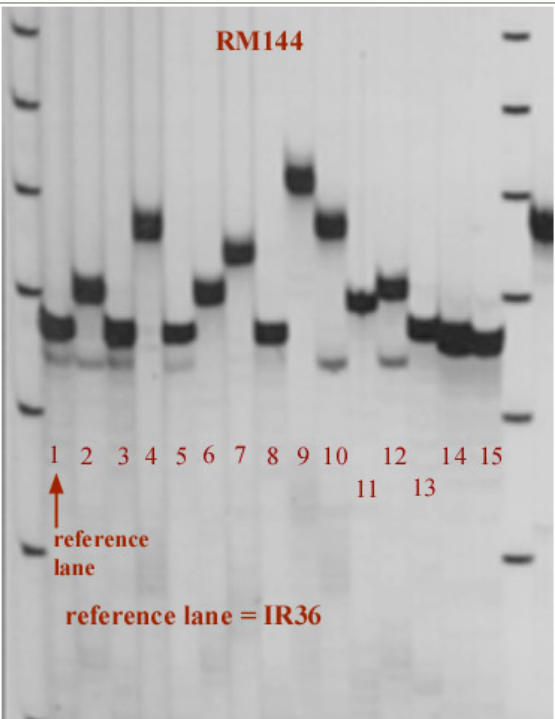
Details	Source/Library	Map Positions	Associations (5)	Images (0)	
Direction	Name	Type	Species	Analysis	Assoc. Type
To	X67711	other_dna	Oryza sativa (indica cultivar-group)	other_dna_poaceae	shared_synonym
From	RM144	SSR Primer Pair	Oryza sativa	primer_pair	primer_pair
From	AUT27367	SSR Primer Pair	Oryza sativa	primer_pair	primer_pair
From	RM144_forward	Primer	Oryza sativa	primer_pair	primer_pair
From	RM144_reverse	Primer	Oryza sativa	primer_pair	primer_pair

Click on the name of the second one (RM144)

### View Rice SSR Primer Pair "RM144"

Details	Source/Library	Map Positions (0)	Associations (2)	Images (1)
ID	6083			
Name	RM144			
Synonyms (1)	GENBANK_ACCESSION <a href="#">X67711</a>			
Type	SSR Primer Pair			
Species	Oryza sativa (Rice)			
Germplasm	Nipponbare			
Description				
Repeat Motif	(ATT)11			
Forward Primer	TGCCCTGGCGCAAATTGATCC			
Reverse Primer	GCTAGAGGAGATCAGATGGTAGTGATG			
Anneal Temperature	55			
Expected PCR Product Size	237			
Remarks				
Sequence Source				

### View Rice SSR Primer Pair "RM144"

Details	Source/Library	Map Positions (0)	Associations (2)	Images (1)
 <p>RM144</p> <p>275</p> <p>250</p> <p>225</p> <p>200</p> <p>175</p> <p>1 2 3 4 5 6 7 8 9 10 12 14 15</p> <p>11 13</p> <p>reference lane</p> <p>reference lane = IR36</p>				
				<p>1 IR36</p> <p>2 N22</p> <p>3 IR64</p> <p>4 Azucena</p> <p>5 Zhai-Ye-Qing 8</p> <p>6 Jing-Xi 17</p> <p>7 Milyang 23</p> <p>8 Gihobyao</p> <p>9 Lemont</p> <p>10 Teqing</p> <p>11 Nipponbare</p> <p>12 Kasalath</p> <p>13 BS125</p> <p>14 BS125/WLO2 F1</p> <p>15 WLO2</p>

➔ 7) Notice the following:

- ➔ a. **Forward and Reverse Primers** – these are the primary defining characteristics of the SSR markers that make it unique. You need to know this if you want to synthesize the primer for yourself.
- ➔ b. **Anneal Temperature** – need to know this to program the PCR
- ➔ c. **Expected PCR Product size** – approximate size of the band that you should expect to see
- ➔ d. **Genome Positions** – click to see marker displayed in the genome browser.
- ➔ e. **Images** – May or may not be available. The images gives a better idea of the range of band sizes on representative germplasm. If you don't see a band in the expected size you may need to adjust your PCR conditions.

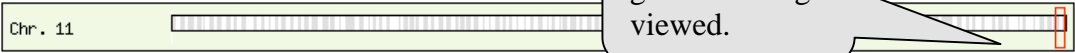
➡ **View RM144 in the Rice Genome Browser**

From #6 above, click on the “Mappings” tab and view RM144 in the Genome Browser. It may take a few moments for the results to load in your browser, but the first thing you will notice is that this marker is located at one end of chromosome 11.

View Rice SSR "RM144"

Details	Source/Library	Map Positions (17)	Associations (5)	Images (0)					
Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Comments	
Oryza sativa (Rice)	Sequence	Class I SSR (93-11) 2005	RM144	11	22,841,290 bp	22,841,552 bp	<a href="#">View Comparative Map</a>		
		Class I SSR (IRGSP) 2005	RM144	11	28,173,807 bp	28,174,051 bp	<a href="#">View Comparative Map</a>		
		Class I SSR (TIGR) 2005	RM144	11	28,158,685 bp	28,158,929 bp	<a href="#">View Comparative Map</a>		
		Gramene Annotated Nipponbare Sequence 2006	RM144	Chr. 11	28,246,911 bp	28,247,155 bp	<a href="#">View in Genome Browser</a>		
			RM144	Chr. 11	28,246,930 bp	28,247,154 bp	<a href="#">View in Genome Browser</a>		
	Genetic	Cornell SSR 2001	RM144	11	123.2 cM	123.2 cM	<a href="#">View Comparative Map</a>		
		IRMI 2003	RM144	11	117.3 cM		<a href="#">View Comparative Map</a>		
	QTL	CNHAU Zhen97/ H94 QTL 2005	RM144	11	141.8 cM	141.8 cM	<a href="#">View Comparative Map</a>		
		CNHAU Zhenshan 97/IRAT109 SSR QTL 2006	RM144	11	121.4 cM	121.4 cM	<a href="#">View Comparative Map</a>		
		CNZU IR1552/Azu RI QTL 2003	RM144	11	17.6 cM	17.6 cM	<a href="#">View Comparative Map</a>		
		CNZU IR1552/Azu RI QTL 2004	RM144	11	17.6 cM	17.6 cM	<a href="#">View Comparative Map</a>		
		Cornell IR64/Azu DH QTL 2001	RM144	11	123.2 cM	123.2 cM	<a href="#">View Comparative Map</a>		
		IRRI RD23/Olong F2 QTL 2003	RM144	11	175 cM	175 cM	<a href="#">View Comparative Map</a>		
		LSU Caiapo/IRGC103544 QTL 2004	RM144	11	77 cM	77 cM	<a href="#">View Comparative Map</a>		
		M202/IR50 UCD QTL 2003	RM144	11	91.5 cM	91.5 cM	<a href="#">View Comparative Map</a>		
		NDSU EM93/SS18 BC QTL 2004	RM144	11	160.3 cM	160.3 cM	<a href="#">View Comparative Map</a>		
		TKU Integrated QTL 2002	RM144	11	131.5 cM	131.5 cM	<a href="#">View Comparative Map</a>		

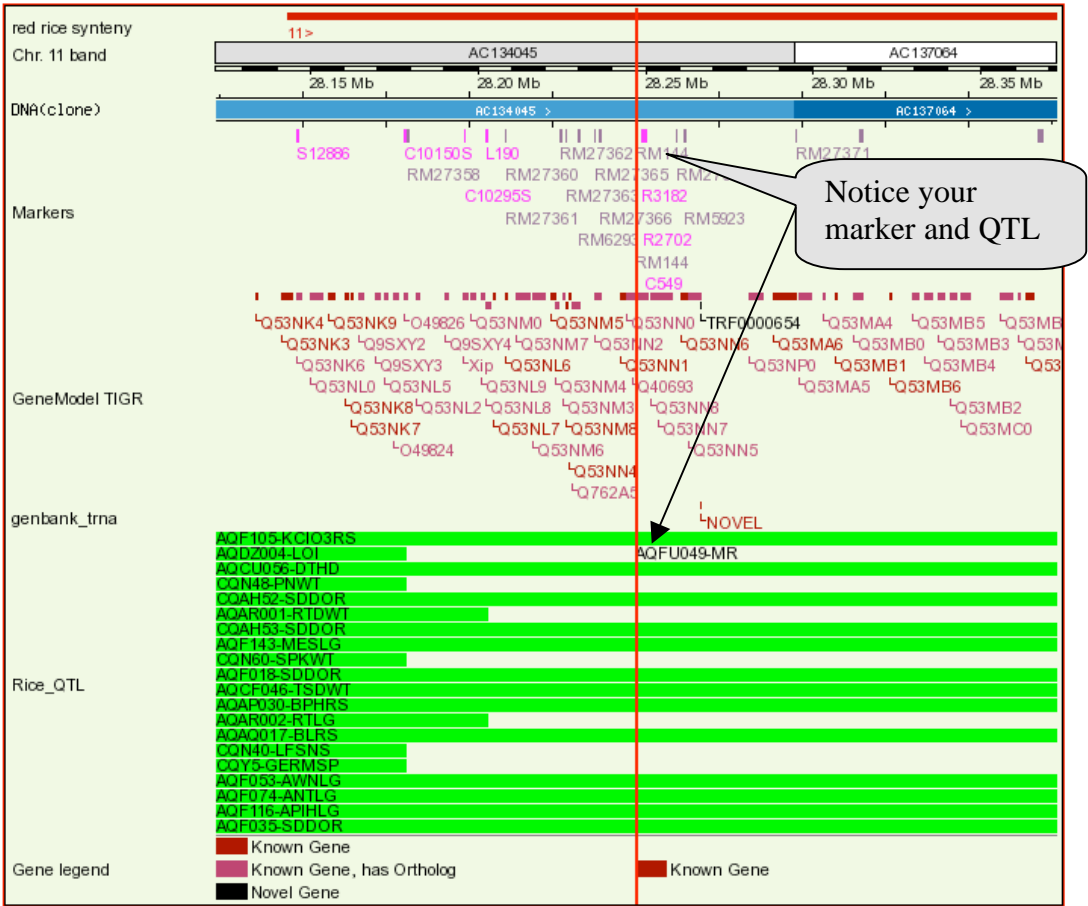
☐ **Chromosome 11**



Red boxes indicate part of genome being viewed.

The “overview” diagram identifies other features mapped to this area, including synteny with other species. This view is magnified from the chromosome view, so along the blue DNA (clone) track there is a box indicating the selected area on the chromosome view.

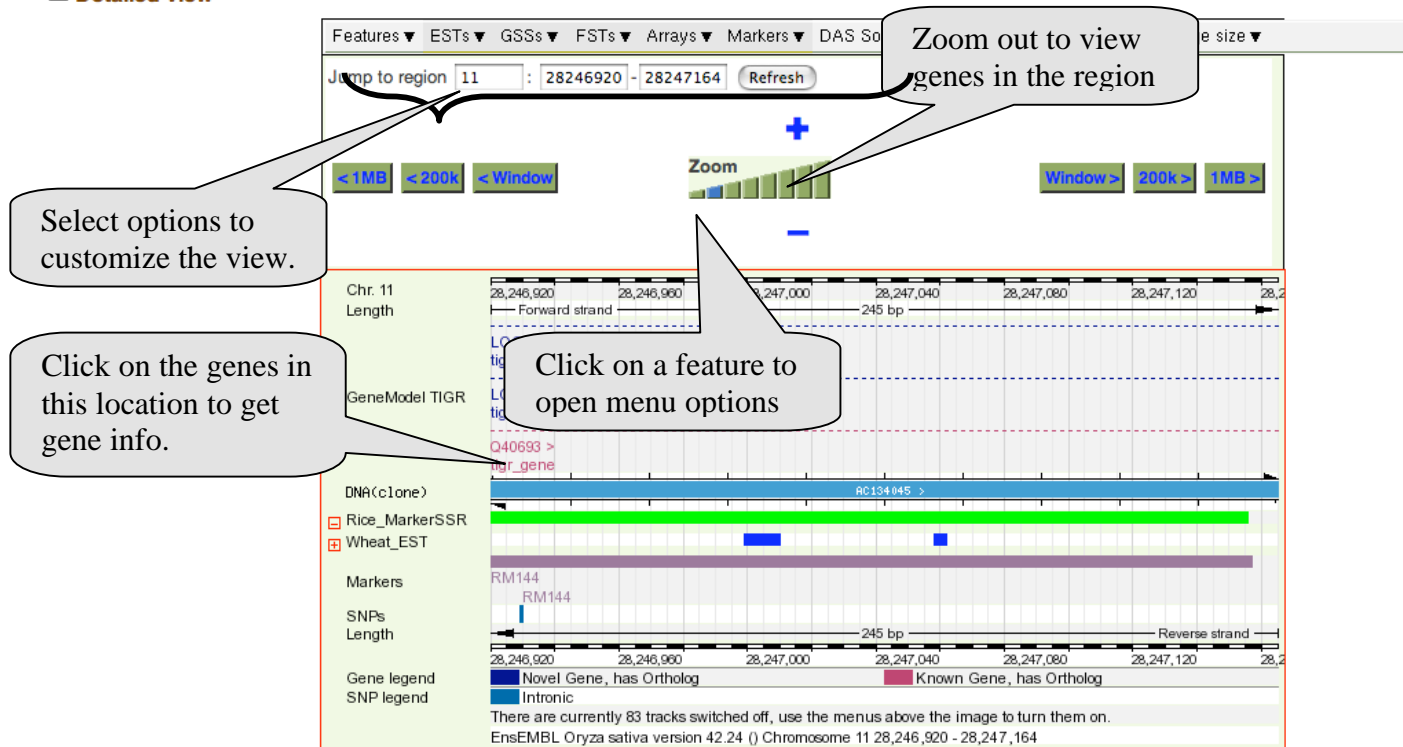
☐ **Overview**





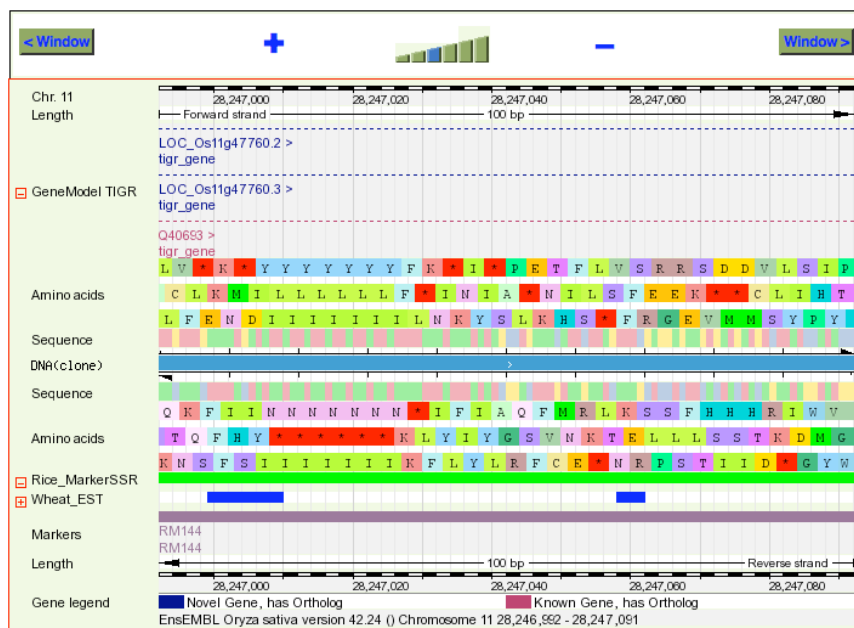
The detailed view is once again magnified from the overview, and zooms in to cover only the area in the selected section of the chromosome. It can be customized to provide information of interest to you by changing the magnification, genomic area, features and decorations through the menus at the top of the display box.

#### Detailed view



Finally, at the bottom of this page you will find the Basepair View. This diagram shows the sequence and the possible codon sequences for this section.

#### Basepair view



In this exercise you have simply begun to learn what Gramene can do. For more complete details on all the features available from each module, review the module tutorials available on the web. Use the feedback button at the top of every page to submit private questions to the Gramene team. The appropriate person will get back to you. For public discussion, join the Gramene listserve.

